

## SI Materials and Methods

### *Mice*

*TPO*<sup>Tg</sup> (1) and *Mpl*<sup>-/-</sup> (2) mice have been previously described. A targeting vector was constructed for generation of a modified *Mpl* allele via homologous recombination in embryonic stem (ES) cells in which an internal ribosome entry site (IRES)-GFP-FRT-PGK-neo-FRT-loxP cassette was inserted immediately downstream of the stop codon in exon 12, along with a loxP site in intron 10 (Fig 1). Chimeric mice were generated from an ES cell clone bearing the targeted locus and heterozygous offspring generated on a C57BL/6 background. The PGK-neo sequence was removed by intercrossing with transgenic mice ubiquitously expressing Flp recombinase (3). The resultant allele acts as a GFP reporter for expression from the *Mpl* locus (*Mpl*<sup>fl/fl</sup>). When bred with deleter cre-expressing mice (4), germline deletion of exons 11 and 12, which encode the intracellular domain of the receptor, results in a null allele (*Mpl*<sup>Delcre/Delcre</sup>). Specific inactivation of *Mpl* in megakaryocytes and platelets (*Mpl*<sup>PF4cre/PF4cre</sup>) was achieved using the previously published *PF4-cre* mice (5). Experiments were performed using procedures approved by The Walter and Eliza Hall Institute of Medical Research Animal Ethics Committee.

### *Haematology and Histology*

Analysis of erythrocytes and platelets for flow cytometry was performed after blood was suspended in buffered saline glucose citrate buffer (116 mM NaCl, 13.6 mM trisodium citrate, 8.6 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.6 mM KH<sub>2</sub>PO<sub>4</sub>, 0.9 mM Na<sub>2</sub>EDTA, 11.1 mM glucose). Single-cell suspensions from bone marrow were prepared in balanced salt solution (0.15 M NaCl, 4 mM KCl, 2 mM CaCl<sub>2</sub>, 1 mM MgSO<sub>4</sub>, 1 mM KH<sub>2</sub>PO<sub>4</sub>, 0.8 mM K<sub>2</sub>HPO<sub>4</sub>, and 15 mM N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid supplemented with 2% [vol/vol] bovine calf serum). Clonal analysis of bone marrow cells (2.5x10<sup>4</sup>) and splenocytes (5x10<sup>4</sup>) was performed in 1 mL semisolid agar cultures of 0.3% agar in Dulbecco/s modified Eagles medium containing 20% newborn calf serum, stem cell factor (100 ng/mL), erythropoietin (2 U/mL), and interleukin-3 (10 ng/mL), incubated at 37°C for 7

days in a fully humidified atmosphere of 10% CO<sub>2</sub> in air. Cultures were fixed, dried onto glass slides, and stained for acetylcholinesterase, Luxol fast blue, and haematoxylin, and the number and type of colonies were determined. Liquid cultures of CD150<sup>+</sup> progenitor cells for megakaryocyte generation was performed in StemPro-34 serum-free medium with nutrient supplement (Invitrogen) and TPO at 200ng/mL. For megakaryocyte ploidy analyses, bone marrow was collected into 1 mL of CATCH buffer (Hank's balanced salt solution with 3% BSA, 1.3 mM sodium citrate, 1 mM adenosine, 2 mM theophylline, and 3% FCS) and stained with FITC-conjugated anti-CD41 antibody (BD Pharmingen) on ice. Samples were incubated with propidium iodide (50 µg/mL in 3.4 mM sodium citrate) for 1 hour on ice, washed twice in CATCH buffer and aggregates were removed with a 100 µm sieve. Samples were treated with 50 µg/mL RNase H for 30 min at room temperature before analysis on a LSRII flow cytometer (Becton Dickinson). Femurs, sternii and spleens were fixed in 10% vol/vol buffered formalin and embedded in paraffin and 1- to 3-µm sections were stained with haematoxylin and eosin for megakaryocyte enumeration via light microscopy. Fluorescence microscopy was performed on individual megakaryocytes stained with Cyto64 (Invitrogen) and analysed using BD Pathway (Becton Dickinson) and Zeiss Live Cell Observer (C4.38, Ziess) with the GFP channel and phase channel.

### ***Flow Cytometry***

Staining was performed using rat anti-mouse biotinylated or fluorochrome-conjugated antibodies specific for Ter119 (Ly-76), Gr1 (Ly6G and Ly6C), Mac1 (CD11b), B220 (CD45R), CD4, CD8, CD41, CD16/32, Sca1 (Ly6A/E), CD48 (BD Pharmingen), cKit (CD117) and CD150 (Biolegend) and IL-7 receptor  $\alpha$  (IL7R $\alpha$ ), CD48, CD105, and CD9 (eBioscience). Secondary staining used streptavidin eFluor450 (BD Pharmingen). Cells were analyzed using a LSR Fortessa flow cytometer (Becton Dickinson), or cells were sorted using a FACS Aria II (Becton Dickinson) flow cytometer after antibody staining with lineage depletion. For analysis of erythroid and platelet reconstitution by sorted progenitors, C57BL/6 mice were exposed to a single dose of 475c Gy of  $\gamma$ -

irradiation, and injected via the tail vein with 1000 progenitor cells sorted from mice expressing the *Aequorea victoria* green fluorescent protein (GFP) protein under the human ubiquitin C promoter, obtained from Jackson Laboratories (Maine, USA) (6). Blood from the tail was analyzed on days 4, 7 and 12 following transplantation.

### ***Western blot analysis***

Protein extracts were prepared from platelets or megakaryocytes in lysis buffer containing 1% (vol/vol) Triton X-100, 50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM EDTA, freshly supplemented with 2 mM Na<sub>3</sub>VO<sub>4</sub>, 10 mM NaF, 1 mM PMSF, and complete protease inhibitor cocktail (Roche Diagnostics) after purification by centrifugation. Proteins were separated by SDS-PAGE using Novex 4-12% Bis-Tris NuPAGE gels, transferred to PVDF membrane. The PVDF membrane was first blocked with 1% BSA in phosphate-buffered saline containing 0.1% Tween 20, and further blocked with the Avidin-Biotin blocking kit from Invitrogen (Cat. No. 00-4303). The membrane was then probed with a biotinylated rat-anti-mouse Mpl mAb (clone AMM2) at 0.5 µg/mL (Cat. No. 10403, Immuno-Biological Laboratories Co., Ltd.), followed by reaction with 1:10,000 diluted NeutrAvidin-HRP (Cat. No. 31030, Pierce). The ECL reaction was performed with Millipore Luminata Forte and the membrane was exposed to Amersham ECL film (GE Healthcare) to visualise endogenous Mpl. The loading control protein β-actin was detected using a goat-anti-actin-HRP from Santa-Cruz.

### ***Platelet life span***

Blood was obtained by cardiac puncture into 0.1 volume of Aster-Jandl anticoagulant (85 mM sodium citrate, 69 mM citric acid, and 20 mg/ml glucose, pH 4.6). Platelet-rich plasma (PRP) was obtained by centrifugation at 125 g for 8 min, followed by centrifugation of the supernatant buffy coat at 125 g for 8 min. Platelets were washed by centrifugation at 860 g for 5 min in 140 mM NaCl, 5 mM KCl, 12 mM trisodium citrate, 10 mM glucose, and 12.5 mM sucrose, pH 6.0 (buffer

A). The platelet pellets were resuspended in PBS and platelets of the same genotype pooled and labeled with biotin (1 $\mu$ g/ml) 1 h at room temperature. The washed platelet pellets were resuspended in a small volume of PBS and platelet counts determined using Sphero blank calibration particles on a FACSCalibur flow cytometer. Platelet counts were adjusted to 2x10<sup>8</sup> cells/ml and 200  $\mu$ l transfused per recipient C57BL/6 mouse (a total of 4x 10<sup>7</sup> cells). Platelets were identified in PRP as being CD41-PE<sup>+</sup> and the proportion of biotinylated (streptavidin-APC<sup>+</sup>) platelets remaining at each time point was assessed. 100% was set based on the mean value of the 1h and 3 h timepoints post transfusion per individual mouse.

### ***Serum TPO measurement***

Mice were bled by cardiac puncture, the blood transferred into BD microtainer serum separator gel tubes (Cat. No. 365968, Becton Dickinson) and allowed to clot at room temperature, and the serum separated by centrifugation. Commercial antibody-based ELISA test kits were used to detect TPO (Mouse Thrombopoietin Quantikine ELISA Kit, MTP00; R&D Systems).

### ***Reverse transcription PCR***

Liver RNA was prepared using Trizol (Life Technologies) according to the manufacturer's instructions and treated with RNase free DNase RQ1 (Promega) and 5 $\mu$ g was used for first strand cDNA synthesis using SuperScript II (Life Technologies). ~0.5 $\mu$ g of cDNA was then used in a Taqman PCR reaction with Universal PCR mastermix and murine TPO (Mm0043704\_m1) and GAPDH (Mm00802090\_m1) Taqman probes (Life Technologies) on an ABI 7900 Fast Real-Time PCR instrument (Applied Biosystems). TPO expression relative to GAPDH control were determined using SDS version 2.3 programme (Applied Biosystems) and expressed as  $\Delta$ CT values.



### ***Statistical Analysis***

Student's unpaired two-tailed t-tests were used using GraphPad Prism v. 5.0a for Mac Os X (GraphPad Software), unless otherwise specified. Bonferroni correction for multiple testing was used where indicated.

### ***LSK global gene expression analysis and bioinformatics***

Total RNA was purified from 400,000 - 500,000 sorted LSK cells using the RNeasy Micro kit (Qiagen). RNA quality was assessed with the Agilent Bioanalyzer 2100 (Agilent Technologies) by using the Agilent RNA 6000 Nanokit (Agilent Technologies) according to the manufacturer's protocol. Up to 200ng of RNA was labelled with standard Total Prep RNA amplification kit (Ambion), and complementary RNA (1.5 µg) was hybridized to illumina Mouse WG-6 V2.0 Expression BeadChips according to Illumina standard protocols. Microarray data were analyzed by using the limma (Version 3.16.5) package of the Bioconductor open-source software project ([www.bioconductor.org](http://www.bioconductor.org)) in R (Version 3.0.1). Raw intensities were normalized by using the neqc function, which performs normexp background correction followed by quantile normalization by using control probes. Probes were filtered if not detected in any sample (detection p value, 0.05). Pairwise comparison was made by using linear modeling and empirical Bayes moderated t statistics and array quality weights (7). The false discovery rate (FDR) was controlled by using the Benjamini-Hochberg algorithm. Probes with  $FDR < 0.05$  were judged to be differentially expressed. Rotational Gene set testing was performed using ROAST, using a set statistic of mean50 whereby significance occurs if greater than 25% of the set are differentially expressed, using gene sets weighted by log fold change, and  $10^4$  rotations (8). Results are displayed using the barcodeplot function in the limma Bioconductor package in R. Gene expression microarray data of CD34<sup>+</sup> bone marrow cells from human patients with essential thrombocythemia were obtained from the Gene Expression Omnibus (GSE9827, (9)), and analysed using affy (Version 1.34.0), rma normalisation, and limma packages in R as described.

## Supplementary Figure and Table Legends

### ***Supplementary Fig. 1. Activity of cre recombinase in PF4-cre mice.***

(A) *PF4-cre* activity indicated by EYFP expression in CD150<sup>hi</sup>CD9<sup>hi</sup> bone marrow megakaryocytes and CD41<sup>+</sup> peripheral blood platelets in *Rosa26EYFP*<sup>PF4cre/PF4cre</sup> (red) mice compared to *Rosa26EYFP*<sup>fl/fl</sup> negative controls (blue), but not in peripheral blood Ter119<sup>+</sup> erythrocytes, or bone marrow Gr1/Mac1<sup>+</sup> myeloid cells, B220<sup>+</sup> lymphocytes, CD4<sup>+</sup> or CD8<sup>+</sup> T-lymphocytes.

(B) Representative flow cytometry profiles of LSK (brown) PreGM (grey), GMP (green), BEMP (purple), CD150<sup>+</sup>CD9<sup>hi</sup> (black) CD150<sup>+</sup>FcγR<sup>+</sup> (red), PreCFU-E (yellow) and CFU-E (orange) cell populations analysed.

(C) Representative plot of EYFP expression (upper panel) in the CD150<sup>+</sup>FcγR<sup>+</sup> progenitor cells in *Rosa26EYFP*<sup>PF4cre/PF4cre</sup> and control *Rosa26EYFP*<sup>fl/fl</sup> mice. Barplot (lower panel) of mean fluorescent intensity (MFI) in arbitrary units of EYFP in defined *Rosa26EYFP*<sup>PF4cre/PF4cre</sup> cell populations relative to *Rosa26EYFP*<sup>fl/fl</sup> controls with standard deviations shown. \* =  $P < 0.02$ .

### ***Supplementary Fig. 2. Characterisation of CD150<sup>+</sup>FcγR<sup>+</sup> progenitor cells.***

(A) Representative flow cytometry plot of Lin<sup>-</sup>Sca-1<sup>-</sup>Kit<sup>+</sup> cells defining the CD150<sup>+</sup>FcγR<sup>+</sup> bone marrow population from a *Mpl*<sup>+/+</sup> mouse. Viable cells per femur shown with standard deviation from n=4 mice at 8-10 weeks of age.

(B) Colony assay of 400 sorted GMP granulomonocytic progenitor and CD150<sup>+</sup>FcγR<sup>+</sup> cells cultured for 7 days in a cytokine cocktail of SCF (100 ng/mL), IL3 (10 ng/mL) and erythropoietin (EPO, 2 U/mL). Blast; blast colony, G; granulocyte, GM; granulocyte-macrophage, M; macrophage, Eo; eosinophil, Meg; megakaryocyte, MegE; megakaryocyte-erythroid, MegI; megakaryocyte-immature, E; erythroid colonies. \* =  $P_{adj} < 0.05$  correction for multiple testing.

(C) Erythrocyte and platelet production from 1000 transplanted CD150<sup>+</sup>FcγR<sup>+</sup> or GMP cells marked with green-fluorescent protein (6) following injection into sublethally irradiated recipient

mice. Platelets and red blood cells were measured at 4, 7, and 12 days following transplantation and cell numbers expressed as the proportion of GFP<sup>+</sup> cells of the total number of platelets or red blood cells shown as a percentage, with 2-3 independent donors and 4 recipients per donor. Mean and standard deviation shown.

***Supplementary Fig. 3. Mpl expression in  $Mpl^{PF4cre/PF4cre}$  mice.***

(A) Expression of the *Mpl-GFP* reporter in  $Mpl^{fl/fl}$  and  $Mpl^{PF4cre/PF4cre}$  megakaryocytes by flow cytometry (upper panel) and live cell imaging (lower panels). Megakaryocytes were generated from Kit<sup>+</sup>Sca-1<sup>-</sup>CD150<sup>+</sup> progenitors cultured in TPO for 4 days. For imaging, individual megakaryocytes were analysed using BD Pathway (Becton Dickinson) and Zeiss Live Cell Observer (C4.38) with GFP channel and phase channel.

(B) Expression of the *Mpl-GFP* reporter in platelets (CD41<sup>+</sup>) and erythrocytes (Ter119<sup>+</sup>) from blood, and in B220<sup>+</sup> B-lymphoid, CD4<sup>+</sup> or CD8<sup>+</sup> T-lymphoid and Gr1/Mac1<sup>+</sup> myeloid cells in the bone marrow of  $Mpl^{fl/fl}$  (red) and  $Mpl^{PF4cre/PF4cre}$  mice (green).  $Mpl^{Delcre/Delcre}$  mice (blue) were included as a negative control.

(C) Representative flow cytometric gating strategy and expression of Mpl in hematopoietic cell populations from  $Mpl^{fl/fl}$  (top panels) and  $Mpl^{PF4cre/PF4cre}$  (bottom panels) mice by flow cytometry using anti-Mpl antibody (red, with isotype control staining in blue).

(D) Representative flow cytometric gating strategy and expression of the *Mpl-GFP* reporter in LSK and progenitor populations in  $Mpl^{fl/fl}$  (red),  $Mpl^{PF4cre/PF4cre}$  (green) and control  $Mpl^{Delcre/Delcre}$  mice (blue).

**Supplementary Fig. 4. Megakaryocytosis, platelet survival curves and platelet half-life in *Mpl*<sup>PF4cre/PF4cre</sup>**

(A) Histological sections of bone marrow from *Mpl*<sup>+/+</sup>, *Mpl*<sup>fl/fl</sup>, *Mpl*<sup>Delcre/Delcre</sup> and *Mpl*<sup>PF4cre/PF4cre</sup> mice. Haematoxylin and eosin staining of representative sections at 200x magnification. Images were acquired with a Zeiss Axioplan-2 microscope 20x/0.30 DIC L objective with AxioCam HrC and AxioVision Version 3.1 image-acquisition software.

(B) Platelets were purified from male *Mpl*<sup>PF4cre/PF4cre</sup> and *Mpl*<sup>fl/fl</sup> control mice, labelled with NHS-biotin and transfused into wild type C57Bl/6 male mice. Platelets were identified as being CD41<sup>+ve</sup> and the proportion of biotinylated (streptavidin<sup>+ve</sup>) platelets remaining at each time point was assessed. n=17 mice received *Mpl*<sup>PF4cre/PF4cre</sup> platelets and n=9 *Mpl*<sup>fl/fl</sup> control platelets. Data is combined from 2 separate experiments and represent mean ± standard deviation.

**Supplementary Fig. 5. Enumeration of progenitor cells in *Mpl*<sup>PF4cre/PF4cre</sup> mice.**

Representative flow cytometry profiles and gating strategies for analysis of cell populations from bone marrow of *Mpl*<sup>+/+</sup>, *Mpl*<sup>fl/fl</sup>, *Mpl*<sup>Delcre/Delcre</sup>, *Mpl*<sup>PF4cre/PF4cre</sup> and *TPO*<sup>Tg</sup> mice. The mean number of each population is shown as viable cells per femur ± standard deviation (*Mpl*<sup>+/+</sup> n= 4, *Mpl*<sup>fl/fl</sup> n=8, *Mpl*<sup>Delcre/Delcre</sup> n=3, *Mpl*<sup>PF4cre/PF4cre</sup> n=6, and *TPO*<sup>Tg</sup> n=5). \* =  $P_{adj} < 0.05$  compared to *Mpl*<sup>fl/fl</sup> and \*\* =  $P_{adj} < 0.05$  compared to *Mpl*<sup>+/+</sup> with correction for multiple testing.

**Supplementary Fig. 6. Recloning potential of *Mpl*<sup>PF4cre/PF4cre</sup> blast colony-forming pre-progenitor cells**

Primary cultures were prepared using 25,000 bone marrow cells from *Mpl*<sup>fl/fl</sup>, *Mpl*<sup>PF4cre/PF4cre</sup> and *TPO*<sup>Tg</sup> mice stimulated with 100ng/mL stem cell factor (SCF) and 100 ng/mL IL-6. Individual primary blast colonies were picked, and replated for 7 days in secondary cultures stimulated by 100 ng/mL SCF, 10 ng/mL IL-3 and 2 U/mL erythropoietin and the type and number of colonies scored after 7 days. The number of colonies of secondary blast, megakaryocyte, granulocyte, granulo-

macrophage, macrophage and eosinophil colonies that developed is shown for 20 ( $Mpl^{fl/fl}$ ,  $Mpl^{PF4cre/PF4cre}$ ) and 40 ( $TPO^{Tg}$ ) independent recloned blast colonies, with the mean number of colonies for each colony type across all three genotypes shown (dotted line). \* =  $P < 0.009$  by Chi-Squared test for proportions using the proportion of colonies greater than the overall mean colony number when comparing  $Mpl^{PF4cre/PF4cre}$  and  $TPO^{Tg}$  primary blast colonies to expected proportions from  $Mpl^{fl/fl}$  primary blast colonies.

***Supplementary Fig. 7. Gene expression changes in CD34<sup>+</sup> cells of patients with essential thrombocythemia***

Barcode plot.  $TPO^{Tg}$  “TPO stimulated” and  $Mpl^{-/-}$  “TPO starved” signature genes (Table S3, S4) can distinguish between CD34<sup>+</sup> bone marrow cells of patients with essential thrombocythemia from controls ((9) GEO database GSE9827,  $P = 8 \times 10^{-4}$ ).  $P$  value derived from rotational gene set testing using ROAST with the  $TPO^{Tg}$  “TPO stimulated” LSK signature and  $Mpl^{-/-}$  “TPO starved” signature weighted by positive and negative log fold-change respectively (see *SI Material and Methods*). Red bars designate upregulated genes in the  $TPO^{Tg}$  “TPO stimulated” LSK signature set; blue bars designate  $Mpl^{fl/fl -/-}$  “TPO starved” LSK signature set.

**Supplementary Table 1.** Immunophenotypic definitions of bone marrow stem and progenitor cell populations.

**Supplementary Table 2.** Differentially expressed genes in  $Mpl^{PF4cre/PF4cre}$  LSKs compared to  $Mpl^{fl/fl}$  LSKs.

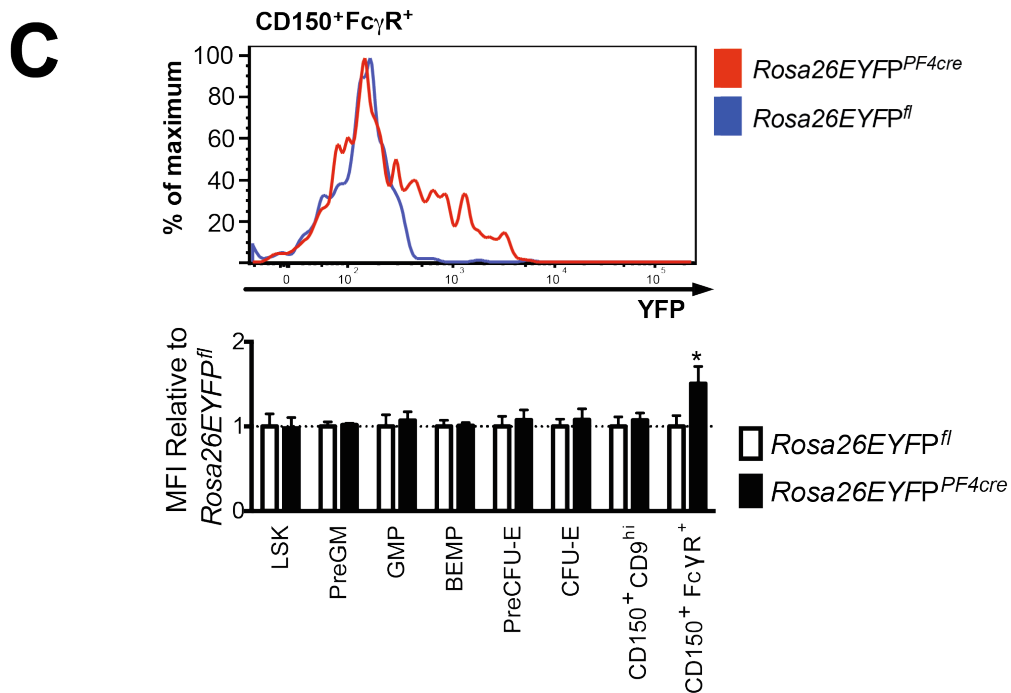
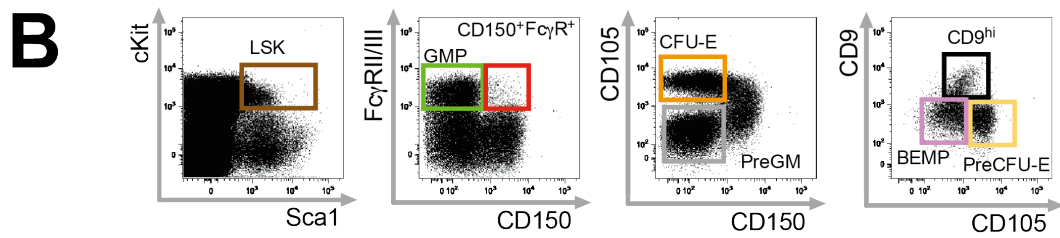
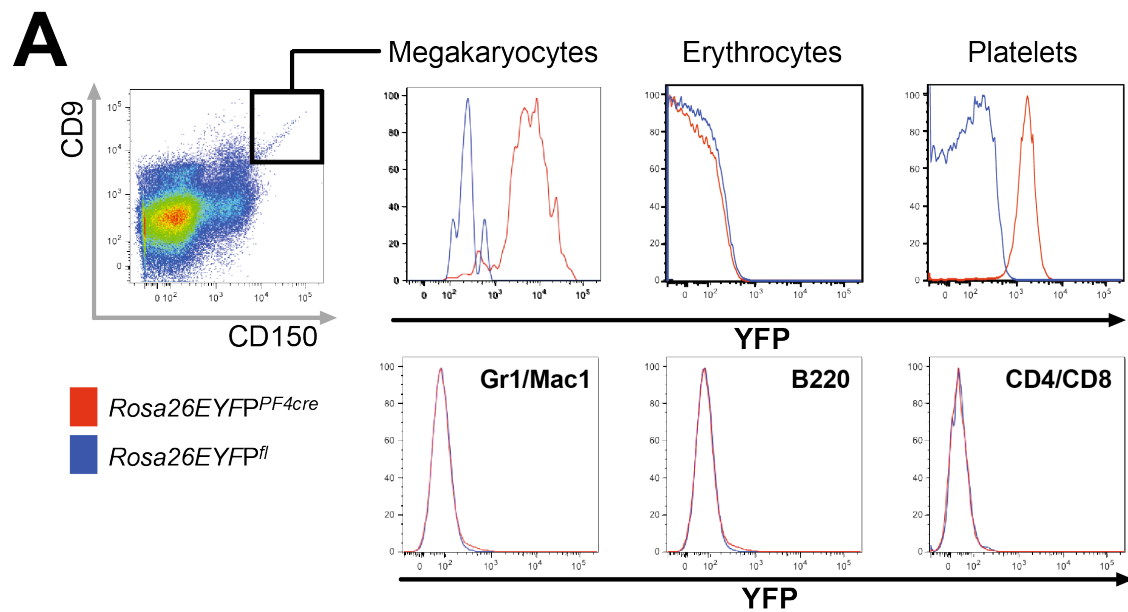
**Supplementary Table 3.** Gene signatures of upregulated genes in  $TPO^{Tg}$  LSKs compared to  $Mpl^{+/+}$  LSKs.

**Supplementary Table 4.** Gene signatures of upregulated genes in  $Mpl^{-/-}$  LSKs compared to  $Mpl^{+/+}$  LSKs.

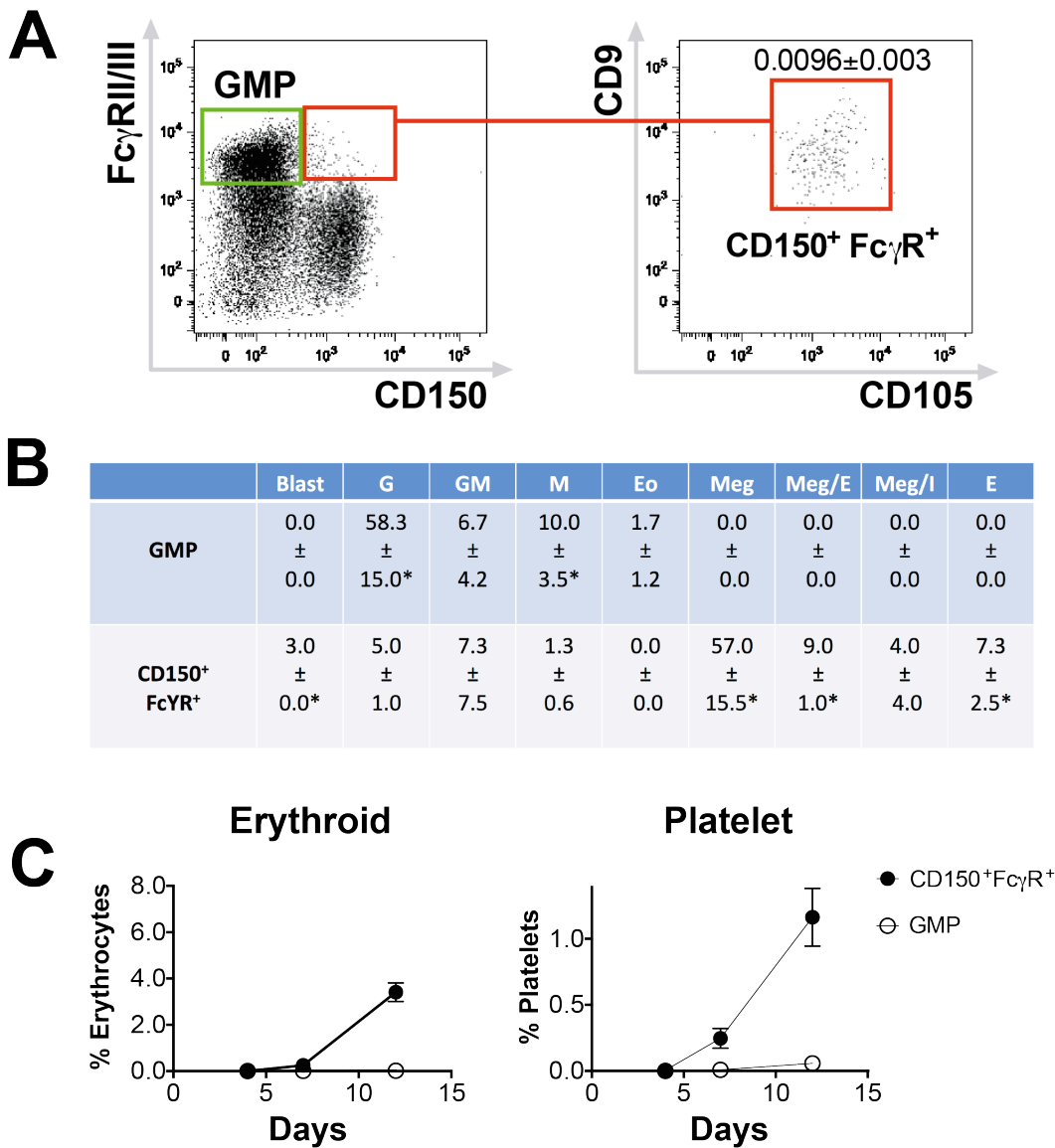
## References

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Supplementary Figure 1

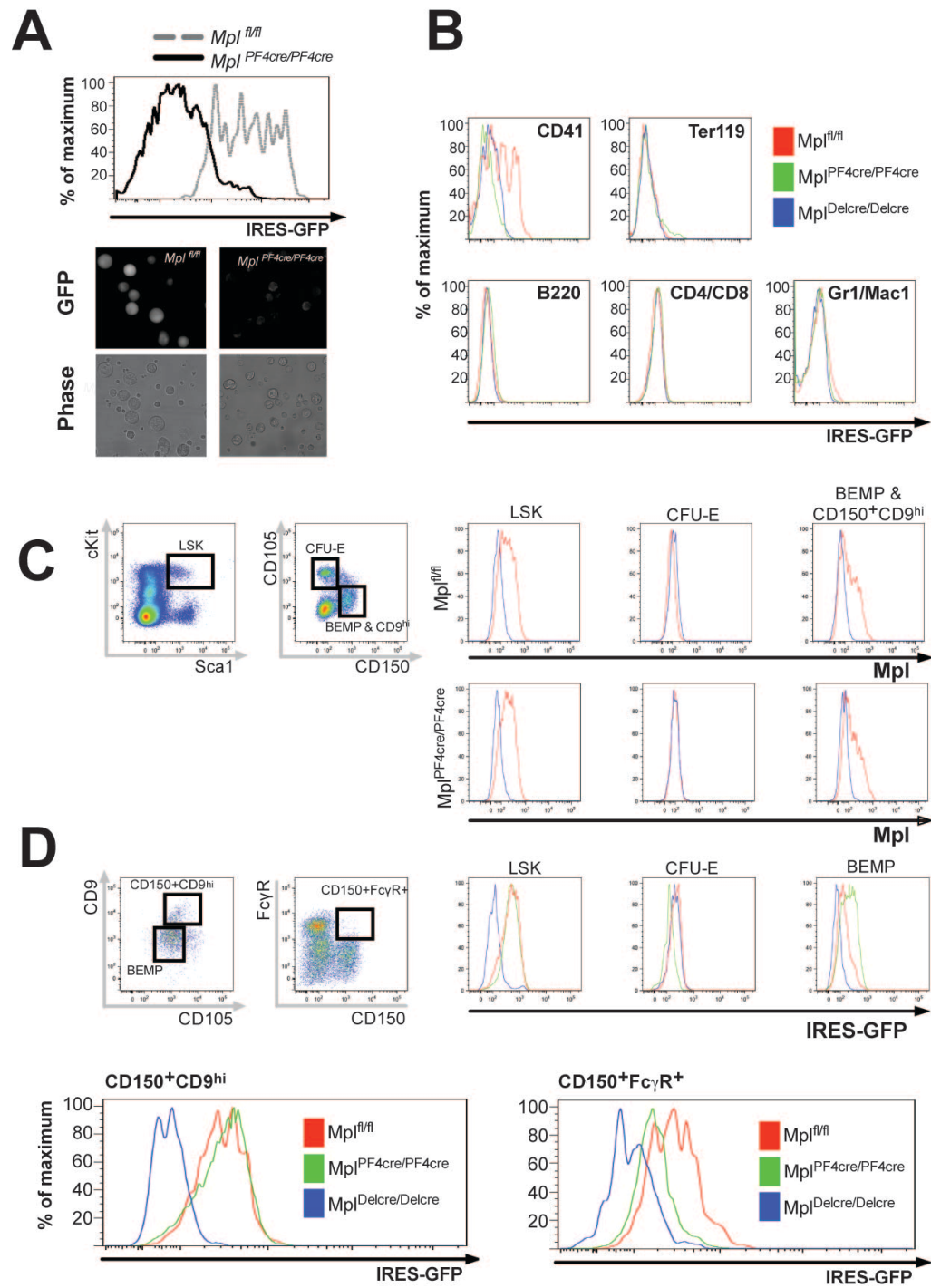


Supplementary Figure 2



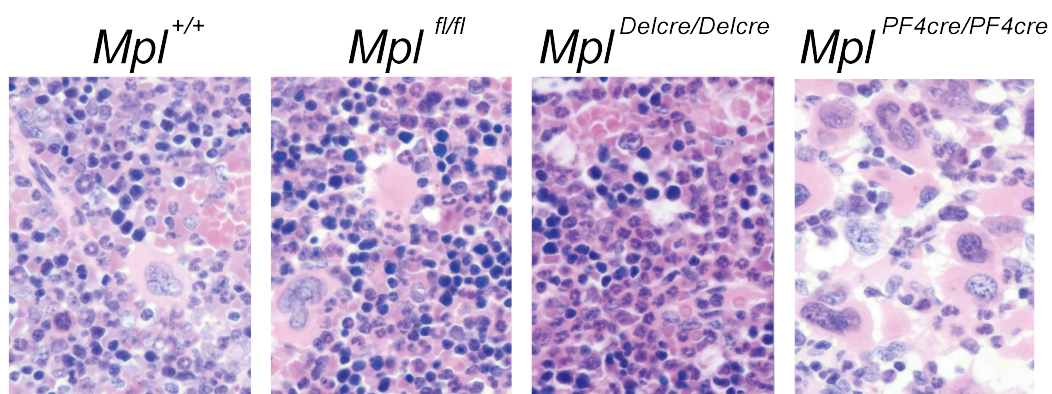


Supplementary Figure 3

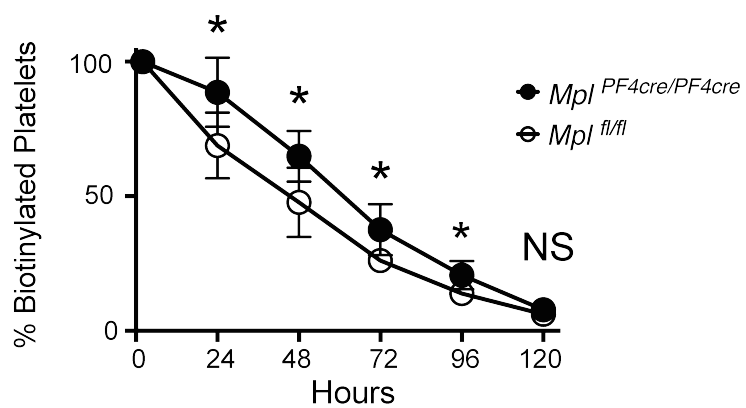


Supplementary Figure 4

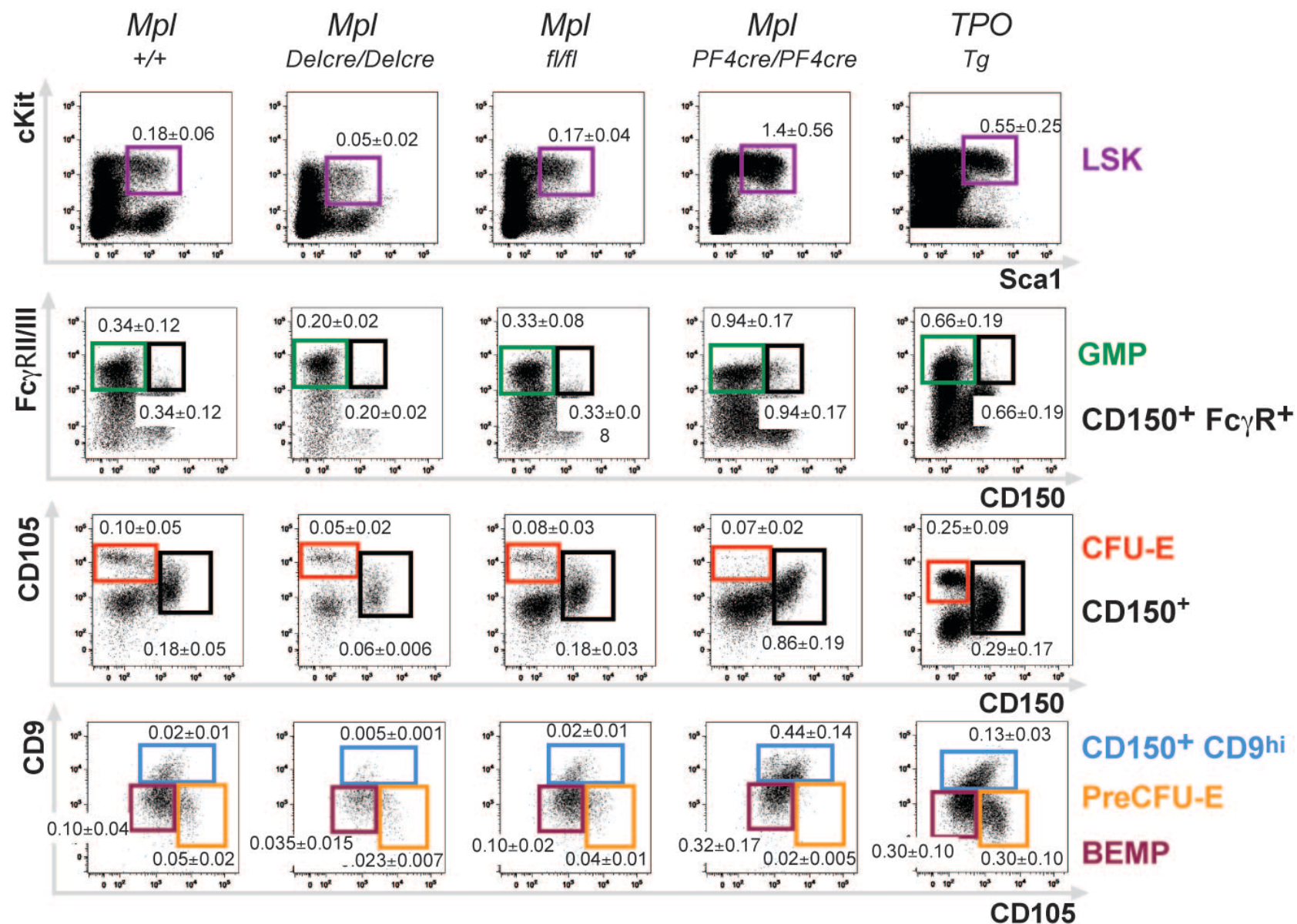
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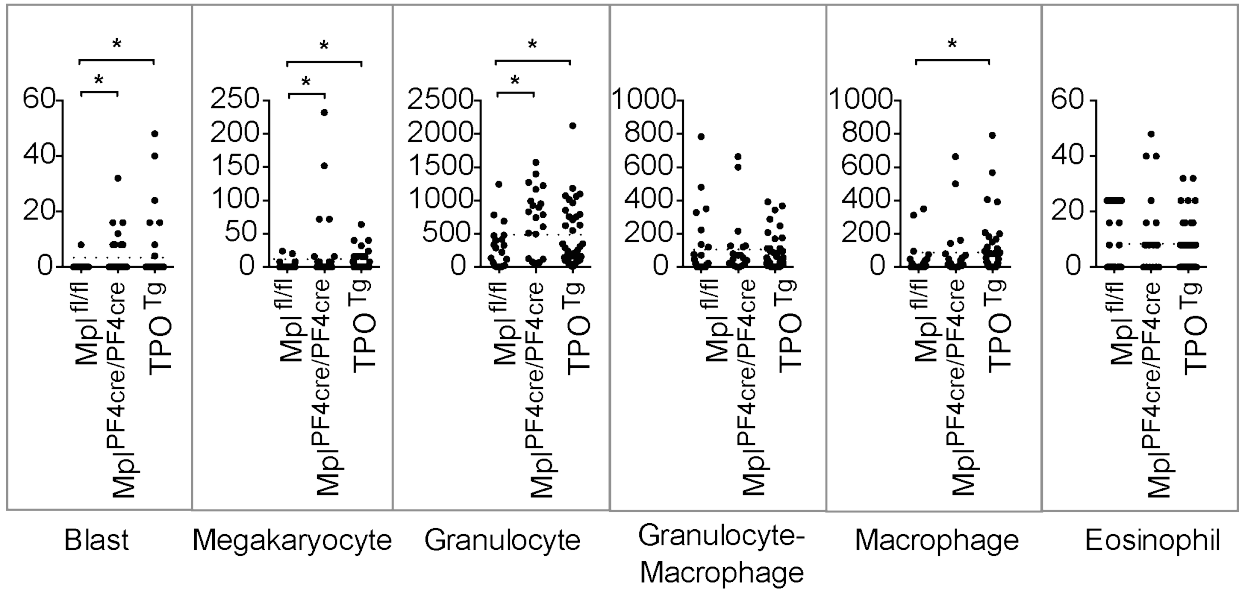
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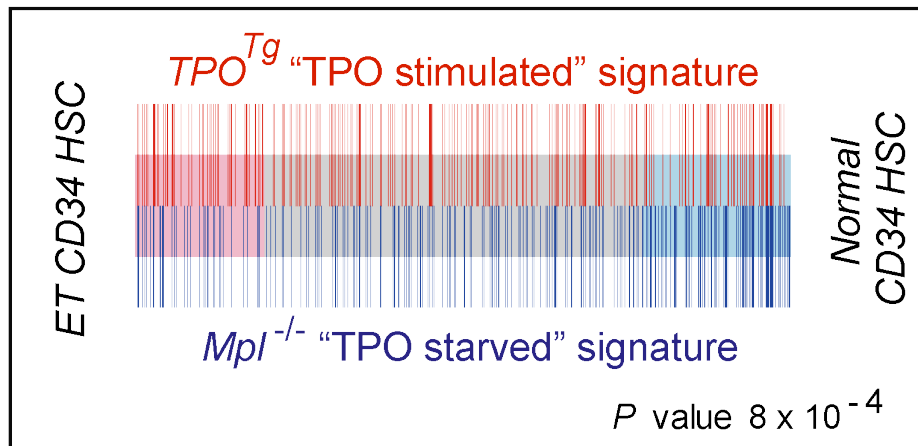
Supplementary Figure 5



Supplementary Figure 6



Supplementary Figure 7



**Supplementary Table 1. Immunophenotypic definitions of bone marrow stem and progenitor cell populations**

<b>Bone Marrow Subset</b>	<b>Immunophenotype</b>
LSK	Lineage <sup>-</sup> Sca-1 <sup>+</sup> Kit <sup>+</sup>
PreGM, pre-granulocyte macrophage	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>-</sup> Endoglin <sup>-</sup> Fc $\gamma$ RII/III <sup>-</sup>
GMP, granulocyte-macrophage	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>-</sup> Endoglin <sup>-</sup> Fc $\gamma$ RII/III <sup>+</sup>
BEMP, bipotential erythroid megakaryocyte	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>+</sup> Fc $\gamma$ RII/III <sup>lo</sup> Endoglin <sup>lo</sup> CD9 <sup>lo</sup>
CD150 <sup>+</sup> CD9 <sup>hi</sup> , CD9 <sup>hi</sup> bipotential erythroid megakaryocyte	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>+</sup> Fc $\gamma$ RII/III <sup>lo</sup> Endoglin <sup>lo</sup> CD9 <sup>hi</sup>
CD150 <sup>+</sup> Fc $\gamma$ R <sup>+</sup> , Fc $\gamma$ RII/III <sup>+</sup> bipotential erythroid megakaryocyte	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>+</sup> Fc $\gamma$ RII/III <sup>+</sup> Endoglin <sup>lo</sup> CD9 <sup>hi</sup>
PreCFU-E, pre-colony forming unit erythroid	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>+</sup> Fc $\gamma$ RII/III <sup>-</sup> Endoglin <sup>hi</sup> CD9 <sup>lo</sup>
CFU-E, colony forming unit erythroid	Lineage <sup>-</sup> IL7R $\alpha$ <sup>-</sup> cKit <sup>+</sup> Sca1 <sup>-</sup> CD150 <sup>-</sup> Fc $\gamma$ RII/III <sup>-</sup> Endoglin <sup>hi</sup>

**Supplementary Table 2:** Gene expression changes in MplPF4/PF4 LSKs versus Mplfl/fl LSKs. This table shows log2 fold changes for genes that are significantly differentially expressed between MplPF4cre/PF4cre LSKs versus Mplfl/fl LSKs. These data were generated from samples which were obtained using the Illumina gene expression platform described in Methods.

ID	GeneRef	Symbol	Log Fold Change
ILMN_2893879	NM_024228.2	GDPD3	4.417589681
ILMN_2806439	NM_182959.2	SLC17A8	4.106250725
ILMN_2628178	NM_007706.3	SOCS2	3.793305954
ILMN_2604494	NM_013723.2	PODXL	3.143256824
ILMN_1249975	XM_001001076.2	IGHG	3.047952954
ILMN_1232989	NM_020578.2	EHD3	2.95407174
ILMN_2742042	NM_019738.1	NUPR1	2.838747695
ILMN_3160292	NM_001013785.2	AKR1C19	2.787071019
ILMN_2519673	NM_011708.3	VWF	2.763435158
ILMN_2931334	NM_021283.1	IL4	2.746914709
ILMN_2731908	XM_358637.1	6330405H19	2.66024107
ILMN_2947526	NM_007899.1	ECM1	2.555062578
ILMN_2772264		IGH-VJ558	2.553948885
ILMN_2735184	NM_009929.2	COL18A1	2.503182448
ILMN_2663403	XM_001481237.1	LOC100043918	2.417915348
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ILMN_2653205	NM_001001999.1	GP1BB	2.352553829
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ILMN_2627920	NM_173014.1	LPCAT2	-2.048662951
ILMN_1229577	NM_009217.1	SSTR2	-2.055873418
ILMN_2715840	NM_007574.2	C1QC	-2.060329847
ILMN_1257143	NM_013848.1	ERMAP	-2.066158116
ILMN_2630939	NM_029810.3	NT5C2	-2.081623446
ILMN_1237948	NM_011570.3	TES	-2.092182845
ILMN_2705407	NM_008774.2	PABPC1	-2.097887993
ILMN_2918479	NM_031165.4	HSPA8	-2.101625294
ILMN_2638299		SLC29A1	-2.104481297
ILMN_2619620	NM_009777.2	C1QB	-2.106746736
ILMN_1218923	XM_001477842.1	LOC100041932	-2.11365358
ILMN_2642913	NM_010128.4	EMP1	-2.118752357
ILMN_2691187	NM_009031.2	RBBP7	-2.128593408
ILMN_2795178	NM_028713.1	RFTN2	-2.132952777
ILMN_2691192	NM_009031.2	RBBP7	-2.150740393
ILMN_1216452	NM_008220.3	HBB-B1	-2.159961014
ILMN_1237186	NM_016907.3	SPINT1	-2.163715428
ILMN_1245354	NM_133211.3	TLR7	-2.168536712
ILMN_1219275	NM_009031.2	RBBP7	-2.19165277
ILMN_2639036	NM_010477.3	HSPD1	-2.193222687
ILMN_1214650	AK012612.1	SCL0002368.1_75	-2.237177115
ILMN_2715601	NM_031158.1	ANK1	-2.259126627
ILMN_2673889	NM_008568.1	MCM7	-2.267351667
ILMN_2589785	XM_001479297.1	LOC100047856	-2.296073636
ILMN_1232884	NM_011451.2	SPHK1	-2.328152612
ILMN_1259714	NM_009873.2	CDK6	-2.380528775

ILMN_1245717	NM_013514.3	EPB4.9	-2.409940403
ILMN_3161601	NM_009221.2	SNCA	-2.416928439
ILMN_2538597	XM_359211.1	LOC386405	-2.453158837
ILMN_1236588	NM_009799.4	CAR1	-2.458210435
ILMN_2629581	NM_009943.2	COX6A2	-2.463360174
ILMN_1252157	XR_001572.1	A330102K04RIK	-2.507418276
ILMN_1215076		F830002E14RIK	-2.523338443
ILMN_2668996	NM_032540.2	KEL	-2.568580257
ILMN_3136638	NM_009221.2	SNCA	-2.58845103
ILMN_2649773	NM_172479.2	SLC38A5	-2.714730423
ILMN_1241039		2510042H12RIK	-2.869452535
ILMN_1241866	NM_033264.1	ARPP21	-2.94504104
ILMN_2718589	NM_007995.3	FCNA	-3.171369477
ILMN_2783997	NM_011280.1	TRIM10	-3.309167116
ILMN_2619200	NM_133245.1	ERAF	-3.427289292
ILMN_1212702	NM_008218.2	HBA-A1	-3.435092798
ILMN_1232383	NM_001043228.1	DNTT	-3.479382529
ILMN_2696696	NM_010369.3	GYPA	-3.678933044
ILMN_2675874	NM_009653.1	ALAS2	-3.869609787
ILMN_1227675	NM_011403.1	SLC4A1	-4.144597802
ILMN_2544056		HBB-B1	-4.436711237
ILMN_1246153	NM_133362.2	ERDR1	-4.990352281
ILMN_2998658	NM_133362.1	ERDR1	-7.268307375



**Supplementary Table 3: Up-regulated gene changes in TPOTg LSKs versus Mpl<sup>+/+</sup> LSKs.** This table shows log2 fold changes for genes that are significantly differentially expressed in a positive direction between TPOTg LSKs versus Mpl<sup>+/+</sup> LSKs. The data were generated from samples which were obtained using the Illumina gene expression platform described in Methods.

ID	GeneRef	Symbol	Log Fold Change
ILMN_1232948		IGKV9-128_AJ231245_I	4.972013053
ILMN_2649286	XM_991819.1	LOC243431	4.19394923
ILMN_2619428	XM_354718.1	IGH-V11	3.81929349
ILMN_2631505	XM_357633.1	LOC384415	3.566487673
ILMN_1217886	XM_984967.1	LOC675759	2.715137492
ILMN_1222734	NM_013467.3	ALDH1A1	2.432020094
ILMN_2628178	NM_007706.3	SOCS2	2.277790566
ILMN_3151149	NM_001033851.1	CPNE8	2.087984108
ILMN_3160292	NM_001013785.2	AKR1C19	1.836371782
ILMN_2931334	NM_021283.1	IL4	1.811199701
ILMN_2731908	XM_358637.1	6330405H19	1.759859519
ILMN_2604494	NM_013723.2	PODXL	1.756310088
ILMN_2771342		FCER1A	1.643621486
ILMN_1226111	XM_001481017.1	LOC100043821	1.547920827
ILMN_2587711	NM_183355.2	PBX1	1.54301509
ILMN_1223708	XM_984967.1	LOC675759	1.518230489
ILMN_2806439	NM_182959.2	SLC17A8	1.508678126
ILMN_1229911	NM_012026.2	RGNEF	1.493088903
ILMN_2619983	NM_008304.2	SDC2	1.481070103
ILMN_1215076		F830002E14RIK	1.467582503
ILMN_2690938	NM_145920.2	EVC2	1.444381066
ILMN_2635895	NM_008880.2	PLSCR2	1.429120305
ILMN_1258914	NM_175328.2	SLC6A15	1.413800115
ILMN_2629591	NM_019734.1	ASAH1	1.393307581
ILMN_2729252	XR_002313.1	5830431A10RIK	1.383100737
ILMN_2467151		CYP11A1	1.367870146
ILMN_2834764	NM_175271.2	GPR23	1.352808109
ILMN_2604501	NM_175526.2	CLEC1A	1.343679073
ILMN_1221341	XR_033502.1	LOC100047226	1.343382684
ILMN_1232600	NM_026301.2	RNF125	1.343279582
ILMN_2742042	NM_019738.1	NUPR1	1.342309114
ILMN_2631892	NM_133880.1	PAFAH2	1.341562663
ILMN_1226921	XM_001006879.1	LOC674004	1.340179367
ILMN_2735184	NM_009929.2	COL18A1	1.338663616
ILMN_2972459	NM_007858.2	DIAP1	1.332704455
ILMN_2759943	NM_011203.2	PTPN12	1.325715686
ILMN_2977404	NM_021883.1	TMOD1	1.323266369
ILMN_1226114	NM_175260.2	MYH10	1.314676885
ILMN_1224339	NM_198295.2	TXNDC10	1.312666767
ILMN_1248202		ARHGEF2	1.306209992
ILMN_2624977		A730024F05RIK	1.298198209
ILMN_2653642	NM_029334.1	ZC3H14	1.27944796
ILMN_2761205	NM_030704.1	HSPB8	1.277743972
ILMN_2599018	NM_013885.2	CLIC4	1.272658602

ILMN_1234126	NM_016893.4	FUT8	1.26780666
ILMN_2641541	NM_007858.2	DIAP1	1.259804125
ILMN_1218024		ARHGEF6	1.250563329
ILMN_2663403	XM_001481237.1	LOC100043918	1.249797013
ILMN_1215651	NM_007671.2	CDKN2C	1.245824747
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ILMN_1225311	NM_010509.1	IFNAR2	1.208625837
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ILMN_3160137	NM_009657.3	ALDOC	1.196677468
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ILMN_1232989	NM_020578.2	EHD3	1.122059156
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ILMN_2562831		CCNI	1.101885817
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ILMN_2681805	NM_010739.1	MUC13	1.020960018
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ILMN_2860242	NM_029436.3	KLHL24	0.990612904
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ILMN_2694175	NM_011925.1	CD97	0.982261802
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ILMN_2939503	NM_153392.1	4922503N01RIK	0.981094598
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ILMN_2745055	NM_080288.1	ELMO1	0.891829663
ILMN_2606746	NM_009801.3	CAR2	0.891584868
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ILMN_2608429	NM_013477.3	ATP6V0D1	0.88577877
ILMN_2627140	XM_283804.7	9830001H06RIK	0.878737171
ILMN_2606601		TGFBR3	0.877542261
ILMN_1217118	NM_032003.1	ENPP5	0.876607849
ILMN_2758878	NM_026432.2	TMEM66	0.876020932
ILMN_2678745	XM_147000.1	2300004C15RIK	0.872082328
ILMN_1224644	NM_013508.1	ELK3	0.870739331
ILMN_2733314	NM_029879.2	RGS7BP	0.863738828
ILMN_3149251	NM_008133.3	GLUD1	0.863554805
ILMN_1250195	NM_008681.2	NDRG1	0.861908015
ILMN_2680054	NM_053078.3	D0H4S114	0.859369488
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ILMN_2937674	NM_198671.1	GSE1	0.849471489
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ILMN_1249863	NM_013730.4	SLAMF1	0.830775099
ILMN_1243082	NM_029679.1	6330500D04RIK	0.830236557
ILMN_2625601	NM_019990.4	STARD10	0.821241182
ILMN_1257107	XM_001481017.1	LOC100043821	0.820249965
ILMN_1226103	NM_027472.2	5730455P16RIK	0.818140556
ILMN_2576336		C130052O15RIK	0.815662291
ILMN_2646166		NDRL	0.811358978
ILMN_2742461		PPP2R5C	0.810430829

ILMN_2717127	NM_172689.3	DDX58	0.809319812
ILMN_2610156	NM_008684.1	NEO1	0.806840973
ILMN_2547482		PIGN	0.806651093
ILMN_2588682	NM_177583.4	APH1B	0.80312906
ILMN_1230878	NM_010395.5	H2-T10	0.802958305
ILMN_1249032	NM_175245.2	2410129H14RIK	0.799524781
ILMN_1219016	NM_133784.2	WWTR1	0.797894135
ILMN_2733492	XM_911470.2	DDHD2	0.791232285
ILMN_1252806	XM_196179.2	LOC268934	0.788624859
ILMN_2822915	NM_172827.1	LNPEP	0.786431999
ILMN_2603647	NM_053109.2	CLEC2D	0.786182833
ILMN_1241414		4930429A08RIK	0.784049385
ILMN_2603888	NM_153392.1	4922503N01RIK	0.78081912
ILMN_2735865	NM_009708.1	RND2	0.778618677
ILMN_1228211	NM_009363.3	TFF2	0.775352011
ILMN_3072337	NM_001033851.1	CPNE8	0.773375736
ILMN_3084087	NM_001039511.1	IVNS1ABP	0.773011153
ILMN_2741277	NM_033174.2	SNURF	0.772665852
ILMN_1241890		KLF7	0.772371677
ILMN_1247017	NM_146112.3	TNRC15	0.767706264
ILMN_2767635	NM_029478.3	TMEM49	0.766003863
ILMN_2460662	NM_009452.1	TNFSF4	0.765551135
ILMN_2749448	NM_153119.2	PLEKHO2	0.762856571
ILMN_2741464	NM_172731.1	FGD5	0.75824002
ILMN_2728521	NM_011421.1	SMPD1	0.756454107
ILMN_1219568	NM_016881.2	PMM2	0.752157619
ILMN_2499305	NM_183355.2	PBX1	0.750493022
ILMN_1213448	XM_976371.1	LOC669658	0.750083039
ILMN_2675000	NM_029070.2	4930511J11RIK	0.747512071
ILMN_2740852	NM_010169.3	F2R	0.746687417
ILMN_2773215	XM_001476174.1	EPB4.1L4B	0.74528881
ILMN_2594419	NM_018771.3	GIPC1	0.745114835
ILMN_1246301	BC019166.1	SCL0002275.1_1	0.744959981
ILMN_2627006	XM_001002157.2	AKAP11	0.74471669
ILMN_2775016		FZD6	0.742970068
ILMN_2445658	XM_913941.2	IGSF10	0.742157852
ILMN_2753077	NM_177231.2	ARRB1	0.741912973
ILMN_2737658	NM_133667.1	PKD2	0.741848927
ILMN_2911344	NM_011636.1	PLSCR1	0.736689155
ILMN_2630827	NM_133858.3	4930504E06RIK	0.734760641
ILMN_2805375	NM_021359.2	ITGB6	0.734530606
ILMN_2791028	NM_007471.2	APP	0.73326377
ILMN_2546905	XM_001472182.1	LOC100044395	0.732803335
ILMN_2734181	NM_019811.3	ACSS2	0.731529997
ILMN_1220243	XM_358834.1	LOC385644	0.726831567
ILMN_2598532	XM_484670.5	EG433144	0.726479933
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ILMN_1252288		2010007H06RIK	0.717614775
ILMN_2687165	NM_018763.1	CHST2	0.716725085
ILMN_2745741	NM_172606.2	MARCH6	0.715353206
ILMN_2751207	NM_008054.1	FYN	0.712266084
ILMN_3072536	NM_173363.4	EIF5	0.709834096
ILMN_3096144	NM_011486.4	STAT3	0.709322574
ILMN_1259749		C030013C21RIK	0.70629528
ILMN_1259022	NM_001081006.1	ETL4	0.705347112
ILMN_2492377	NM_023230.2	UBE2V1	0.702840196
ILMN_2648661	NM_007598.2	CAP1	0.696491287
ILMN_2440059	AF390178.1	SCL0001533.1_63	0.695952576
ILMN_1224116	NM_020561.2	SMPDL3A	0.693185833
ILMN_2701271	NM_011636.1	PLSCR1	0.690385083
ILMN_2742942	NM_026817.3	RABL2A	0.688989161
ILMN_1233752	NM_001083341.1	MBOAT2	0.687754382
ILMN_3160863	NM_026725.2	DUSP23	0.687337528
ILMN_1233678	NM_008364.1	IL1RAP	0.687105176
ILMN_2482766	NM_009433.2	TSPYL1	0.685720464
ILMN_2632206	NM_022000.2	GNAS	0.683679627
ILMN_1220813	NM_001013371.2	DTX3L	0.683247642
ILMN_2600053	NM_024211.2	SLC25A11	0.675066375
ILMN_2544674		2310045K21RIK	0.673445392
ILMN_1231254	NM_008007.1	FGF3	0.672987267
ILMN_1224714	XM_988632.2	LOC634731	0.672072555
ILMN_1222036	NM_027995.2	PAQR7	0.669326032
ILMN_2775064	XM_001476174.1	EPB4.1L4B	0.667740253
ILMN_2612283	NM_008090.4	GATA2	0.665968293
ILMN_2772248		CAPNS1	0.65282083
ILMN_2728796	NM_181344.4	C1RL	0.649191621
ILMN_2604256	XM_485050.5	LOC433464	0.64087111
ILMN_3145814	NM_001081079.1	OGFRL1	0.64037838
ILMN_3064669	NM_001045483.1	MAPK1IP1	0.639987385
ILMN_1248622		E130309K17RIK	0.63627387
ILMN_2993836	NM_016747.2	DLG3	0.633779412
ILMN_1253986	XM_981375.2	DLG5	0.630556447
ILMN_2776304	NM_011591.4	TIMM17B	0.628616652
ILMN_2752873	NM_010708.1	LGALS9	0.627603438
ILMN_1227460		2700089E24RIK	0.623093477
ILMN_2594205	NM_026033.1	GATAD1	0.622279026
ILMN_2710705	NM_011018.2	SQSTM1	0.617360312
ILMN_1260417		4732423C17RIK	0.606078652
ILMN_2568516		RBPMS	0.602146442
ILMN_2541190	XM_912953.3	1500034J01RIK	0.601681471
ILMN_1235494	NM_025439.2	TMEM9	0.599091563
ILMN_2678400	NM_133766.1	C920006C10RIK	0.597595002
ILMN_1232099	NM_019793.2	TSPAN3	0.594479725
ILMN_2725617	NM_008439.3	KHK	0.594341099
ILMN_2717251	NM_001080818.1	CDC14A	0.593492261
ILMN_2454204		TNFRSF22	0.587235888
ILMN_3115162	NM_001048177.1	JAK2	0.57914893

ILMN_2461320		AU020206	0.571697356
ILMN_2972063	NM_027086.1	UBL7	0.568169554
ILMN_2615601	NM_028776.4	SCYL3	0.56574517
ILMN_1221458	NM_029074.2	TMEM188	0.564610489
ILMN_2693679	NM_183115.3	CCDC125	0.557220908
ILMN_2557387		E430005I09RIK	0.554483981
ILMN_2607786	NM_146094.1	FADS1	0.553221073
ILMN_2741465	NM_172731.2	FGD5	0.547589158
ILMN_2501489	NM_009515.1	WAS	0.54142052
ILMN_1249219		2310011G17RIK	0.532749488
ILMN_3105205	NM_001039533.1	PDXDC1	0.532169838
ILMN_1257193	NM_008910.2	PPM1A	0.531819674
ILMN_2667618	NM_017478.2	COPG2	0.531419618
ILMN_2810882	NM_008908.1	PPIC	0.530813312
ILMN_2710338	NM_013582.2	LHCGR	0.527886694
ILMN_2794825	NM_153083.2	THTPA	0.525598901
ILMN_2520326		NBEA	0.524175352
ILMN_2676876	NM_145630.2	PDK3	0.521026545
ILMN_1232025	NM_028036.3	TMCO6	0.518542572
ILMN_2680142	NM_009673.1	ANXA5	0.511801841
ILMN_1233970	NM_177231.2	ARRB1	0.509746762
ILMN_1249882	XM_127578.2	4933425A18RIK	0.508812639
ILMN_2592093	NM_018854.3	IFT20	0.507159841
ILMN_1219067	NM_146115.3	A830007P12RIK	0.501599084
ILMN_1256354	NM_008129.3	GCLM	0.491216735
ILMN_2686125	NM_145426.2	MFAP3	0.488744476
ILMN_1237670	NM_009849.1	ENTPD2	0.487284744
ILMN_1256012	NM_181326.3	ZFP521	0.484513737
ILMN_2683128	NM_009908.1	CMAS	0.481153337
ILMN_2745036	NM_024191.1	ARL2BP	0.480691504
ILMN_1238436	NM_009946.2	CPLX2	0.4791412
ILMN_1220569		5730589K01RIK	0.476387925
ILMN_2606243	NM_016891.3	PPP2R1A	0.448658977
ILMN_2760979	NM_009371.2	TGFB2	0.44361108
ILMN_3135697	NM_181274.3	1200003I07RIK	0.410837435
ILMN_2511953	NM_134131.1	TNFAIP8	0.404735242

**Supplementary Table 4:** Up-regulated gene changes in Mpl<sup>-/-</sup> LSKs versus Mpl<sup>+/+</sup> LSKs. This table shows log2 fold changes for genes that are significantly differentially expressed in a positive direction between Mpl<sup>-/-</sup> LSKs versus Mpl<sup>+/+</sup> LSKs. These data were generated from samples which were obtained using the Illumina gene expression platform described in Methods.

ID	GeneRef	Symbol	Log Fold Change
ILMN_2998658	NM_133362.1	ERDR1	8.954391785
ILMN_1246153	NM_133362.2	ERDR1	6.816476343
ILMN_3159435	NM_183151.1	MID1	5.084532231
ILMN_2617920	NM_028624.1	1110017D15RIK	4.197388718
ILMN_2536068	XM_357269.1	LOC383809	2.525455242
ILMN_2705166	NM_145933.3	ST6GAL1	1.994772367
ILMN_1238102		IDE	1.992559259
ILMN_2648661	NM_007598.2	CAP1	1.930166378
ILMN_1240317		A430059D01RIK	1.872659459
ILMN_2619452	NM_010797.1	MID1	1.826208065
ILMN_1232383	NM_001043228.1	DNTT	1.777905687
ILMN_1257143	NM_013848.1	ERMAP	1.691793303
ILMN_2629581	NM_009943.2	COX6A2	1.661529528
ILMN_2680827	NM_008372.3	IL7R	1.654416671
ILMN_1241866	NM_033264.1	ARPP21	1.61123036
ILMN_1215076		F830002E14RIK	1.582448448
ILMN_1223539	NM_001001491.1	TPM4	1.468819636
ILMN_2624977		A730024F05RIK	1.43964822
ILMN_2837396	NM_001005788.2	ZFP69	1.432101011
ILMN_2606825	NM_007717.1	CMAH	1.429516631
ILMN_1252488	NM_020257.1	CLEC2I	1.418652116
ILMN_2653642	NM_029334.1	ZC3H14	1.395674153
ILMN_2582171		A630098G22RIK	1.385791604
ILMN_2746283	NM_194464.2	MRVI1	1.372190135
ILMN_2680737		GRIA2	1.364734143
ILMN_1226921	XM_001006879.1	LOC674004	1.351829981
ILMN_2705196	NM_001008549.1	BC043301	1.341363717
ILMN_1225311	NM_010509.1	IFNAR2	1.328769361
ILMN_2939503	NM_153392.1	4922503N01RIK	1.322898072
ILMN_3103575	NM_001012451.1	ANKRD6	1.312720773
ILMN_2639036	NM_010477.3	HSPD1	1.312272254
ILMN_1245354	NM_133211.3	TLR7	1.309355795
ILMN_2673566	NM_010124.2	EIF4EBP2	1.298915756
ILMN_1216546	NM_027121.2	VKORC1L1	1.293619373
ILMN_2797973	NM_008828.2	PGK1	1.29214651
ILMN_2804559	NM_178638.2	TMEM108	1.251887697
ILMN_2683718	NM_028233.2	LRPPRC	1.248314477
ILMN_1218024		ARHGEF6	1.244257571
ILMN_1224339	NM_198295.2	TXNDC10	1.24367764
ILMN_2571492		IQGAP1	1.243456866



ILMN_1256084		PPP1R1C	1.242746907
ILMN_2637113	NM_177909.2	SLC9A9	1.242563514
ILMN_3126646	NM_130891.1	GRIP1	1.242348791
ILMN_2515273	NM_011978.2	SLC27A2	1.228755015
ILMN_1215280	XM_128487.2	LOC224732	1.218953225
ILMN_1249305	XR_002517.1	LOC209281	1.218535511
ILMN_2599018	NM_013885.2	CLIC4	1.216499038
ILMN_1235833	XM_001480577.1	ZFP422-RS1	1.216062842
ILMN_1254898		9830004G04RIK	1.200026963
ILMN_3107690	NM_028527.1	1700047I17RIK1	1.195357688
ILMN_2712498	NM_001013368.4	E2F8	1.192450161
ILMN_2827588	NM_010029.1	DDX4	1.185990185
ILMN_2852380	NM_011899.3	SRP54	1.184837968
ILMN_2538277	XM_359103.1	LOC386168	1.173251513
ILMN_1245292	NM_019869.2	RBM14	1.160948046
ILMN_1217302	NM_009211.2	SMARCC1	1.151013811
ILMN_1260417		4732423C17RIK	1.145011853
ILMN_2613313	NM_177727.4	LSM14B	1.144092645
ILMN_2541584	XM_356181.1	LOC382100	1.127807852
ILMN_1242700	NM_029701.1	SPCS3	1.119718647
ILMN_1258474	NM_177389.3	MIA3	1.116037902
ILMN_2653681	NM_023858.2	MTMR2	1.113866616
ILMN_2526382	XM_355225.1	LOC381285	1.110758233
ILMN_1236349	NM_027946.3	WDR68	1.106436766
ILMN_2669912	NM_008737.1	NRP1	1.094169732
ILMN_2510683	NM_145441.3	UBXD4	1.093876554
ILMN_1244600	NM_001040396.2	2810407C02RIK	1.08790631
ILMN_2704496	NM_198607.1	4930572J05RIK	1.08507662
ILMN_2477213	XM_001473915.1	LOC100045240	1.07337191
ILMN_2606564	NM_026195.2	ATIC	1.063774536
ILMN_2505307	NM_013771.4	YME1L1	1.059853008
ILMN_2745480	NM_010200.2	FGF13	1.053988916
ILMN_1250501	NM_010147.3	EPN1	1.050451213
ILMN_1247030		PPP1R1C	1.049169655
ILMN_2684268	NM_145926.2	MGAT4B	1.045829879
ILMN_1227464		9930122J16RIK	1.041627805
ILMN_2558167		9330158N06RIK	1.026989272
ILMN_1227671	NM_013496.2	CRABP1	1.025562462
ILMN_2728729	NM_011521.2	SDC4	1.019791198
ILMN_3114998	NM_001008549.1	BC043301	1.018647343
ILMN_2827267	NM_001003666.2	ZFP457	1.018635921
ILMN_1232165	XM_138691.2	MGC60742	1.014698608
ILMN_1216412	NM_010247.2	XRCC6	1.012481692
ILMN_1259419	XM_914270.2	CNOT1	1.009831609
ILMN_2675223	NM_021293.2	CD33	1.006608872
ILMN_2759943	NM_011203.2	PTPN12	1.005607675

ILMN_2642913	NM_010128.4	EMP1	1.001191353
ILMN_2908022	NM_172405.1	CCDC98	0.998936686
ILMN_1240752		A630054N20RIK	0.992305888
ILMN_2621122	NM_180600.2	UBE2Q2	0.987930807
ILMN_2740568	NM_008173.3	NR3C1	0.986999688
ILMN_1255419		ZFPN1A1	0.986153188
ILMN_1253996	NM_054089.2	NCOA6IP	0.983052076
ILMN_2689473	NM_007381.3	ACADL	0.979763368
ILMN_1248202		ARHGEF2	0.978071702
ILMN_2745055	NM_080288.1	ELMO1	0.977738251
ILMN_2528860	XM_354869.1	LOC380959	0.971197971
ILMN_1259769	NM_008774.2	PABPC1	0.970076677
ILMN_1234336	NM_139117.2	CSDA	0.963301688
ILMN_2616768	NM_029478.3	TMEM49	0.962685453
ILMN_1220441	NM_177343.3	CAMK1D	0.961394255
ILMN_3042324	NM_001013391.1	CPSF6	0.960385419
ILMN_2702374	NM_177167.4	PPM1E	0.954696238
ILMN_2560602	XM_001001363.1	CENTD1	0.951532838
ILMN_1252806	XM_196179.2	LOC268934	0.947131193
ILMN_2822915	NM_172827.1	LNPEP	0.944986953
ILMN_2774140	NM_013686.3	TCP1	0.944597633
ILMN_2603976		F730031O20RIK	0.941059287
ILMN_1236599	XR_032463.1	LOC546090	0.934540891
ILMN_1231873	NM_019770.2	TMED2	0.932848282
ILMN_2670662	NM_144901.2	CSDE1	0.930986399
ILMN_2509139	NM_028173.3	TRAM1	0.929278817
ILMN_1247460	NM_133752.2	OPA1	0.927043166
ILMN_2720836	NM_178446.2	RBM47	0.925172154
ILMN_2739651	NM_009688.1	BIRC4	0.923579927
ILMN_1246359	XR_033125.1	LOC100047009	0.921286623
ILMN_2606567	NM_026195.1	ATIC	0.918191469
ILMN_2625058	NM_133714.4	2310037I24RIK	0.91565254
ILMN_2711615	NM_008362.1	IL1R1	0.912557911
ILMN_2671984	NM_011210.2	PTPRC	0.912523101
ILMN_2544674		2310045K21RIK	0.9103057
ILMN_2759944	NM_011203.2	PTPN12	0.908174219
ILMN_2432039	NM_198416.1	ZZZ3	0.90415063
ILMN_2687602	NM_011138.1	POU2F2	0.903955631
ILMN_1257279	NM_172120.3	VPS41	0.900574169
ILMN_2529490	NM_001033634.2	ZYG11B	0.8978995
ILMN_2692484		KLHL5	0.897207477
ILMN_2499888	NM_198416.2	ZZZ3	0.894707926
ILMN_2603888	NM_153392.1	4922503N01RIK	0.892687625
ILMN_1240218	NM_018889.2	PIGB	0.884798627
ILMN_2539454	XM_001479143.1	LOC100042952	0.884754349
ILMN_2658827	NM_139299.1	IL31RA	0.883469869

ILMN_2648047	XM_357858.1	2010309E21RIK	0.883356903
ILMN_2675239	NM_001009949.1	MCART1	0.882312243
ILMN_2908687	NM_207246.2	RASGRP3	0.880725418
ILMN_3034034	NM_028527.1	1700047I17RIK1	0.879208365
ILMN_2547482		PIGN	0.877999893
ILMN_2640789	NM_177547.3	SGK3	0.874702855
ILMN_2620934	XM_910859.3	MACF1	0.870321996
ILMN_1251169	XM_130859.4	4631434O19RIK	0.868594619
ILMN_1260372	NM_013753.1	X99384	0.865108178
ILMN_2750098	NM_134078.3	CHMP7	0.86456254
ILMN_1230221	NM_133714.4	2310037I24RIK	0.861566284
ILMN_2471289	NM_020267.2	TRIM44	0.861076287
ILMN_1233545	NM_029999.3	LBH	0.861074793
ILMN_1256395		E130208E03RIK	0.860794153
ILMN_2736168	NM_008917.2	PPT1	0.859469016
ILMN_1224653	XR_032194.1	LOC432730	0.858481732
ILMN_2985484	NM_001081411.1	SCLT1	0.857688179
ILMN_3149251	NM_008133.3	GLUD1	0.855971494
ILMN_2736762	NM_025903.1	IFRD2	0.855923634
ILMN_3122922	NM_001039195.1	GRIA2	0.85371629
ILMN_3065373	NM_198607.1	4930572J05RIK	0.852667766
ILMN_1229577	NM_009217.1	SSTR2	0.85189457
ILMN_1227627	NM_025999.1	RNF141	0.851877098
ILMN_2753979	NM_001039103.2	RASA4	0.848149629
ILMN_2691567	NM_026601.1	HYI	0.846487793
ILMN_2676074	XM_001479341.1	LOC100047905	0.842065643
ILMN_3094853	NM_008863.3	PKIB	0.841073969
ILMN_1229687	NM_025999.2	RNF141	0.838273871
ILMN_2497067	NM_144516.1	ZMYND11	0.837702178
ILMN_2606990	NM_023066.2	ASPH	0.836516995
ILMN_2595732	XM_001475817.1	LOC100046232	0.826229618
ILMN_1246301	BC019166.1	SCL0002275.1_1	0.826149947
ILMN_1251750		2810031B20RIK	0.825088528
ILMN_2440059	AF390178.1	SCL0001533.1_63	0.823118423
ILMN_1216239	NM_001081213.1	ERMP1	0.822502205
ILMN_2815802	NM_199302.1	LRSAM1	0.820939132
ILMN_2715304	NM_026267.1	NECAP1	0.818511919
ILMN_1217931	NM_009462.1	USP10	0.817847516
ILMN_2610309	XR_033125.1	LOC100047009	0.817844084
ILMN_2598532	XM_484670.5	EG433144	0.815089713
ILMN_2428782		SCL0003328.1_225	0.814668948
ILMN_2651137	NM_010693.1	LCK	0.812483415
ILMN_1237527	NM_021525.2	RCL1	0.806676499
ILMN_2966162	NM_178936.3	TMEM56	0.805142089
ILMN_2742778	NM_028032.1	PPP2R2A	0.804296532
ILMN_2610771	NM_001047159.1	NET1	0.80242051

ILMN_2626547	NM_016881.2	PMM2	0.802294425
ILMN_1223044	XM_976860.1	LOC665427	0.801291854
ILMN_1219304	NM_001012638.1	ACD	0.801143178
ILMN_1219568	NM_016881.2	PMM2	0.79984672
ILMN_1217993	NM_080471.2	ANKRD6	0.798933767
ILMN_1251995		TTLL4	0.791708548
ILMN_3138674	NM_009637.3	AEBP2	0.791563144
ILMN_2733492	XM_911470.2	DDHD2	0.791435921
ILMN_1259075	NM_138314.2	NME7	0.786759788
ILMN_2598402	NM_001081009.1	PARP8	0.785653511
ILMN_2745614	NM_025459.2	1810015C04RIK	0.784128923
ILMN_1230959	NM_001005788.2	ZFP69	0.781921179
ILMN_2890515	NM_008741.1	NSG2	0.781337001
ILMN_3106388	NM_001080118.1	MED1	0.780852261
ILMN_2699645	NM_194054.2	RTN4	0.780435701
ILMN_2626252	NM_007717.1	CMAH	0.780192599
ILMN_1216473	NM_029582.2	TXNDC11	0.780179687
ILMN_2677712	NM_007480.1	ARF5	0.779482235
ILMN_2674351	NM_010332.2	EDNRA	0.777633218
ILMN_2728584	XM_128981.2	HAK-PENDING	0.777566477
ILMN_2970879	NM_016723.1	UCHL3	0.777270172
ILMN_1241414		4930429A08RIK	0.775163191
ILMN_2681604	NM_001038998.1	CCDC23	0.774397218
ILMN_2797061	NM_033268.3	ACTN2	0.768861742
ILMN_2680540	NM_011829.2	IMPDH1	0.763560256
ILMN_2454204		TNFRSF22	0.76326443
ILMN_1259133		9430088P09RIK	0.763153572
ILMN_1251005	NM_026942.2	STOML1	0.761324698
ILMN_2630459	NM_009911.2	CXCR4	0.759063092
ILMN_1222385	NM_145436.2	CDC27	0.75803625
ILMN_1215434	NM_013910.2	FBXL10	0.757685804
ILMN_1245979	XM_355907.1	LOC381891	0.756748447
ILMN_1213014	NM_009471.2	UMPS	0.746768701
ILMN_1259905	NM_001093753.1	SFRS11	0.746033582
ILMN_1231181	NM_025664.5	SNX9	0.744773212
ILMN_1240537	NM_028755.2	ARPP21	0.744756813
ILMN_1259754	NM_011278.3	RNF4	0.740110101
ILMN_1222243	NM_148928.1	GTF3C5	0.739510291
ILMN_2606072	NM_010472.2	HRB	0.736097141
ILMN_1246471	NM_009431.2	CTR9	0.73377977
ILMN_3102035	NM_010488.3	ELAVL4	0.733742371
ILMN_1246034	NM_153160.3	ZCCHC17	0.7325241
ILMN_2506144	NM_019806.5	VAPB	0.731825205
ILMN_2759945	NM_011203.2	PTPN12	0.731561435
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ILMN_1232495	XM_001471637.1	LOC100044177	0.667981728
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